

SEQUENCE LISTING

<110> Thomas, Christopher
 McPherson, Michael
 Atkinson, Howard
 Neelam, Anil

<120> Plant Cell Death System

<130> 9341-027

<150> 0025225.4
 <151> 2000-10-14

<160> 18

<170> PatentIn Ver. 2.1

<210> 1
 <211> 909
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)..(48)
 <223> N-terminal Domain

<220>
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 <222> (865)..(903)
 <223> C-terminal Domain

<220>
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 <222> (484)..(558)
 <223> Central Domain

<220>
 <221> mutation
 <222> (226)..(231)
 <223> Sequence replacing removed SacI site

<220>
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 <222> (1)..(3)
 <223> Initiation codon added via PCR primer

<220>
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 <222> (904)..(909)
 <223> Stop codons added via PCR primer

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 <222> (1)..(24)
 <223> Binding site for primer ProRIPBF

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<220>
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<222> (205)..(249)
<223> Binding site for primer RIPSDF

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<222> Complement((205)..(249))
<223> Binding site for primer RIPSDF

<220>
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<222> Complement((880)..(909))
<223> Binding site for primer ProRIPSR

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<222> (49)..(73)
<223> Binding site for primer RIP1BF

<220>
<221> misc_feature
<222> Complement((837)..(864))
<223> Binding site for primer RIP2SR

<220>
<221> misc_feature
<222> (463)..(579)
<223> Binding site for primer RIPCDF spanning central
domain

<220>
<221> misc_feature
<222> Complement((463)..(579))
<223> Binding site for primer RIPCDF spanning central
domain

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<400> 1
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gcgtcggtcc ggaagacgt gatcaaacac tgcaccgacc ataaagggat cttccagccc 180
gtgctgccac cggagaagaa ggtcccggag ctatggttct acacagaact gaaaactagg 240
accagctcca tcacgtcgc catcgcgatg gacaacctgt acctcgtggg cttcaggacc 300
cggggcgggg tgtggtggga gttcggcaag gacggcgaca cccacctctc cggcgacaac 360
cccaggtggc tcggtctcgg cggcaggtac caggacctca tcggcaacaa gggctcggag 420
accgtacca tgggcgcgc cgaatgacc agggccgtca acgacctggc gaagaagaag 480
aagatggcga cactggagga ggaggagggt aagatgcaga tgcagatgcc ggaggccgct 540
gatctggcgg cggcggcgag ggctgaccca caggccgaca cgaagagcaa gctggtgaag 600

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ctgtgtgtca tgggtgtcga ggggtgcgg ttcaacaccg tgtcccgac ggtggacgcg 660
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 tgggacagga tctccaagcg ggccttcgag tgggctgacc accccaccgc tgtgatcccc 780
 gacatgcaga agcttggcat caaggataag aacgaagcag cgaggatcgt tgcgctcggt 840
 aagaatcaaa ctactgccgc tgccgctact gctgccatg ctgacaacga cgacgacgag 900
 gcctaataa 909

<210> 2
 <211> 750
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> Initiation codon added via PCR primer

<220>
 <221> mutation
 <222> (181)..(186)
 <223> Sequence replacing removed SacI site

<220>
 <221> misc_feature
 <222> (745)..(750)
 <223> Stop codons added by PCR primer

<400> 2
 atgaaaagaa tagtgccaaa gtctactgaa atcttccccg tggaggacgc gaactaccct 60
 tacagcgctt tcatcgcgct ggtccggaag gacgtgatca aacactgcac cgaccataaa 120
 gggatcttcc agccccgtgtt gccaccggag aagaaggctc cggagctatg gttctacaca 180
 gaactgaaaa ctaggaccag ctccatcacg ctgccatac gcattggaca cctgtacctc 240
 gtgggcttca ggacccccgg cgggggtgtg tgggagtctg gcaaggacgc cgacaccacc 300
 ctctctggcg acaacccccg gtggctcgcc ttccggcgga ggtaccagga cctcatcgcc 360
 aacaagggtc tggagacctt caccatgggc cgcgccgaaa tgaccaggcc cgtcaacgac 420
 ctggcgaaag agaagaagcg ggtgaccca caggccgaca cgaagagcaa gctggtgaag 480
 ctggtgtgtca tgggtgtcga ggggtgcgg ttcaacaccg tgtcccgac ggtggacgcg 540
 ggggttcaaca gccagcacgg ggtgaccttg accgtgacgc aggggaagca ggtgcagaag 600
 tgggacagga tctccaagcg ggccttcgag tgggctgacc accccaccgc tgtgatcccc 660
 gacatgcaga agcttggcat caaggataag aacgaagcag cgaggatcgt tgcgctcggt 720

<210> 3
 <211> 444
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> Initiation codon added by PCR primer

<220>
 <221> mutation
 <222> (181)..(186)
 <223> Sequence replacing removed SacI site

<220>
 <221> misc_feature
 <222> (439)..(444)
 <223> Stop codons added by PCR primer

<400> 3
 atgaaaagaa tagtgccaaa gttcactgaa atcttcccg tggaggagcg gaactaccct 60
 tacagcgctc tcatcgctc ggtccggaaa gacgtgatca aacactgcac cgaccataaa 120
 gggatcttcc agcccggtgct gccaccggag aagaaggtec cggagctatg gttctacaca 180
 gaactgaaaa ctaggaccag ctccatcacg ctcgccatac gcatggacaa cctgtacctc 240
 gtgggcttca ggaccccggtg cgggggtgtgg tgggagtctg gcaaggacgg cgacacccc 300
 ctctcggcg acaaccccag gtggctcggc ttcggcgcca ggtaccagga cctcatcgcg 360
 aacaagggtc tggagacctg caccatgggc cgcgccgaaa tgaccagggc cgtcaacgac 420
 ctggcgaaga agaagaagta ataa 444

<210> 4
 <211> 354
 <212> DNA
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> Initiation codon added by PCR primer

<220>
 <221> misc_feature
 <222> (349)..(354)
 <223> Stop codons added by PCR primer

<400> 4
 atggcggtg accccacaggc cgacacgaag agcaagctgg tgaagctggt ggtcatgggtg 60
 tgcgaggggc tgcggttcaa caccgtgtcc cgcacggtgg acgcgggggt caacagccag 120
 cacgggggtga ccttgaccgt gacgcagggg aagcaggtgc agaagtggga caggatctcc 180
 aaggcggcct tcgagtgggc tgaccacccc accgctgtga tccccgacat gcagaagctt 240
 ggcatacaag ataagaacga agcagcgagg atcggtgcgc tcgtaagaa tcaactact 300
 gccgctgccg ctactgctgc cagtgtgtac aacgacgacg acgaggccta ataa 354

<210> 5
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ProRIPBF
 primer

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

<400> 5
 actcgagtct agaggatcca tggccgagat aaccctagag ccg 43

<210> 6
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ProRIPSR
 primer

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

<400> 6
 gactagtgtc gacgagctct tattaggcct cgtogtcgtc gttgtcagc 49

<210> 7
 <211> 47
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: RIP1BF primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 7
gctcgagtct agaggatcca tgaaaagaat agtgccaaag ttcactg
47

<210> 8
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP2SR primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 8
gactagtgtc gacgagctct tattaggcag cggcagtagt ttgattotta acg
53

<210> 9
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP1SR primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 9
aactagtgtc gacgagctct tattacttct tcttcttcgc caggctcgtt acg
53

<210> 10
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIP2BF primer

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<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 10
actcgagtct agaggatcca tggcggctga cccacaggcc gacacgaaga g      51

<210> 11
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIPCDF primer

<400> 11
gacctggcga agaagaagaa ggcggctgac ccacaggccg ac      42

<210> 12
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIPCDR primer

<400> 12
gtcggcctgt gggtcagccg ccttcttctt cttcgccagg tc      42

<210> 13
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RIPSDF primer

<220>
<221> mutation
<222> (22)..(27)
<223> Nucleotides modified to remove SacI site

<400> 13
cggagctat ggtttacac agaactgaaa actaggacca gctcc      45

<210> 14
<211> 45
<212> DNA
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: RIPSDR primer

 <220>
 <221> mutation
 <222> (19)..(24)
 <223> Nucleotides modified to remove SacI site

 <400> 14
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 <210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: SUB21 primer

 <400> 15
 ctcttgcttg aattcggact a 21

 <210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: SUB25 primer

 <400> 16
 tagtccgaat tcaagcaaga gcaca 25

 <210> 17
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: LDT15 primer

 <400> 17
 gacagaagcg gatccttttt tttttttttt 30

 <210> 18
 <211> 381
 <212> DNA
 <213> Nicotiana tabacum

<400> 18
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 atataactta gtcgtctcaa ttaaacatt aatgtgaaat ataatcaaa aaaagccaaa 120
 gggcgggtggg acggcgccaa tcatttgtcc tagtcactc aaataaggcc catggtcggc 180
 aaaaccaaac acaaaatgtg ttatttttaa tttttctctc ttttattgtt aaagttgcaa 240
 aatgtgttat ttttggttag accctatgga tatataaaga caggttatgt gaaacttgga 300
 aaacatcaa gttttaagca aaaccctctt aagaacttaa attgagcttc ttttgggca 360
 tttttctagt gagaaggatc c 381